

**Multiple Alignment:**

30664188.0.99	1	MHR L I F V Y T L I C A N F C S C R D T S A T P Q S A S I K A L R N A N L R R D E S N H L T D L Y R R D E T I Q V K G	60
VEGF-E	1	--MSLFGLLLTSLAAGRQGTQAESNLSSKQFSSNK---EQNGVQDPQ-HERIITWST	54
30664188.0.99	61	NGYVQS PRFPNS YPRNLLLTWR LHS-QENTRIQLVFDNQFGLLEAEENDICRYDFVEVEDI	119
VEGF-E	55	NGSIHSPRPHTWPRTVLVWR LVAEENWWIQLT FEDEREGLEDPEDDICKYDFVEVEEP	114
30664188.0.99	120	SETSTIRGRWCGHKEWPPRIKSR TNQIKITFKSDDWFAKPGEKIYYSLL EDFOPAAS	179
VEGF-E	115	SDG--TILGRWCGSGTWPGKQISKGNQIRIRFVSDEWFPSFEGFCIHNI VMP-----	165
30664188.0.99	180	ETNWESVTSSI SGWSYNPSPVTDPT-LTIADA LDKKIAEFDTVEDILKVFNPE SWQEDLEN	238
VEGF-E	166	-----QFTEAVS-----PSVLPPSALPLDLLNNAITAFSTLEDLIRMLEPERWQDLED	214
30664188.0.99	239	MYLDTPRYRGRSYHD-RKS-KVDLDRLNDDAKRYSCTPRNYSVNI REELKL ANVVFFPRF	296
VEGF-E	215	LVRPTWQLLGKAFVFGRKSHVVDLNLLTEEVRLYSCTPRNFVSIREELKRTDTIFWPGF	274
30664188.0.99	297	LLVQR CGGCNCGGCTVNWRSC TNSGKTVMKKYHEVLQFEPGHIKRRGRAKTMA LVDIQLDH	356
VEGF-E	275	LLVKRCGGNCACCLHNCNEQQVP SKVTMKYHEVLQLRP---KTGV RGLHK SLTDVA LEH	331
30664188.0.99	357	HERCDCISSSRPPR	(SEQ ID NO:2) 370
VEGF-E	332	HEECDCV ERGSTGG	(SEQ ID NO:28) 345

FIG. 2.

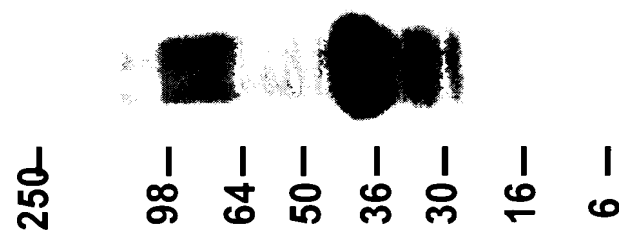


FIG. 3.

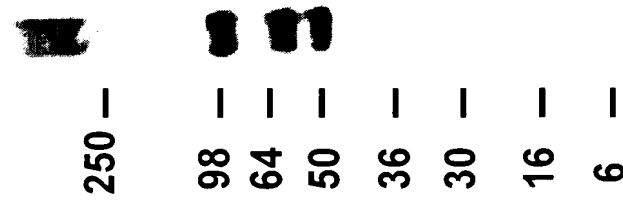


FIG. 4A

IgK      30664188      V5    His



aa 24-370

293 Transfection

Ni Affinity Chromatography

Imidazole Elution

FIG. 4B

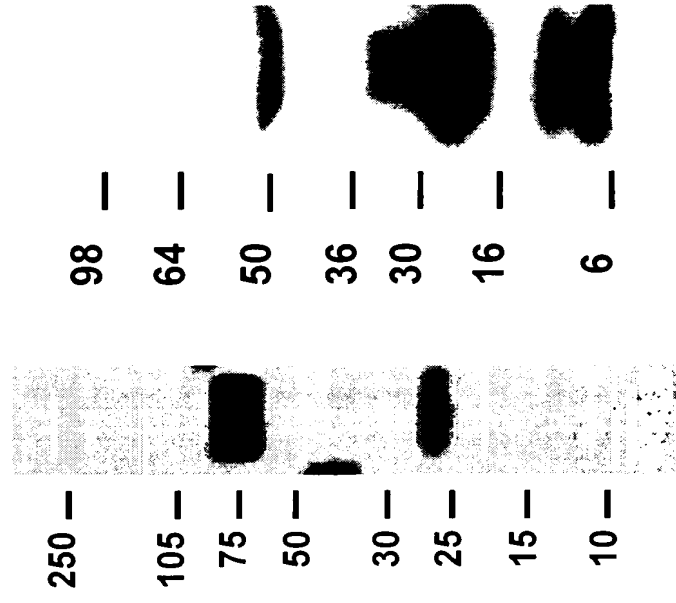


FIG. 5.

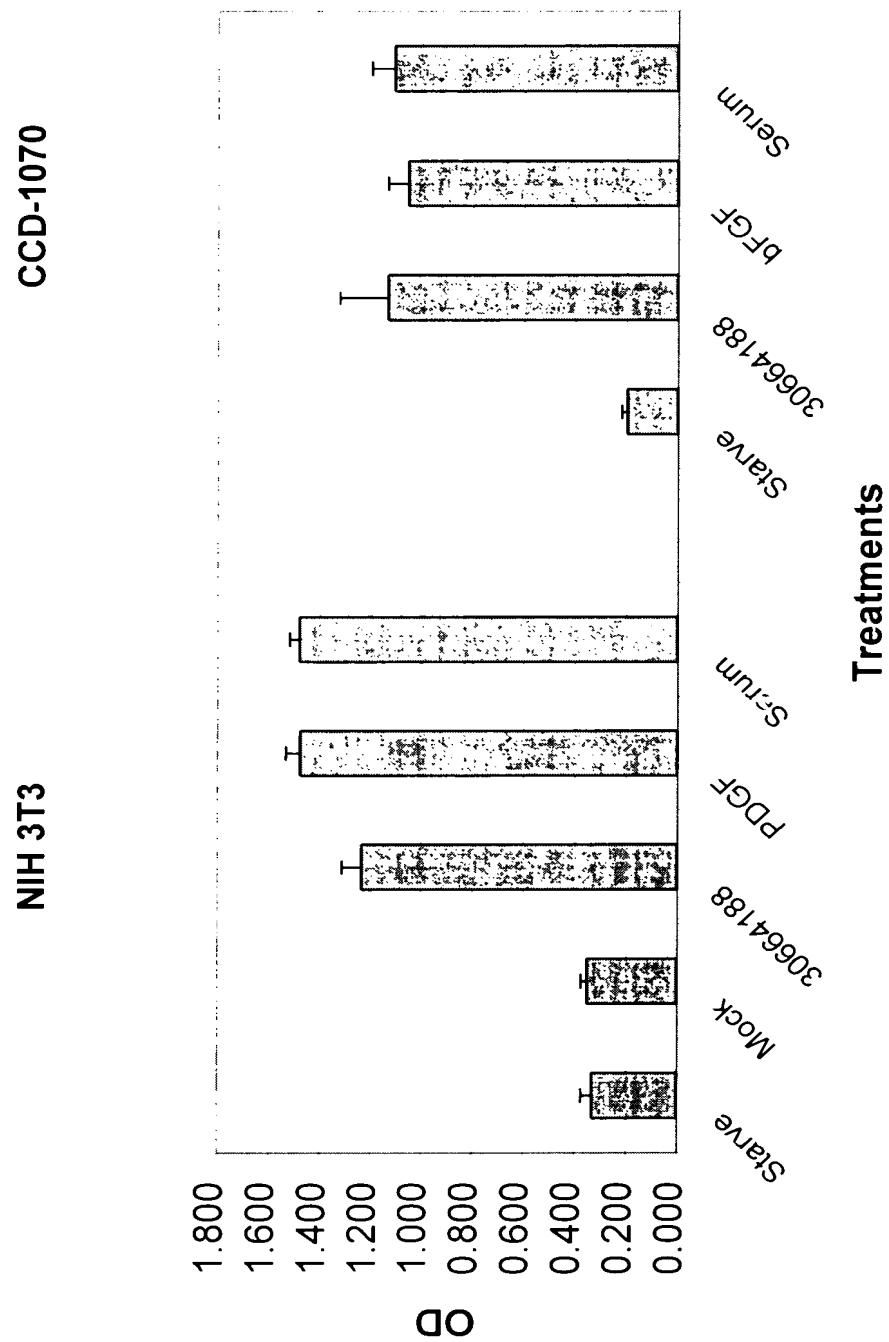


FIG. 6.

BrdU Proliferation NIH 3T3 5-24

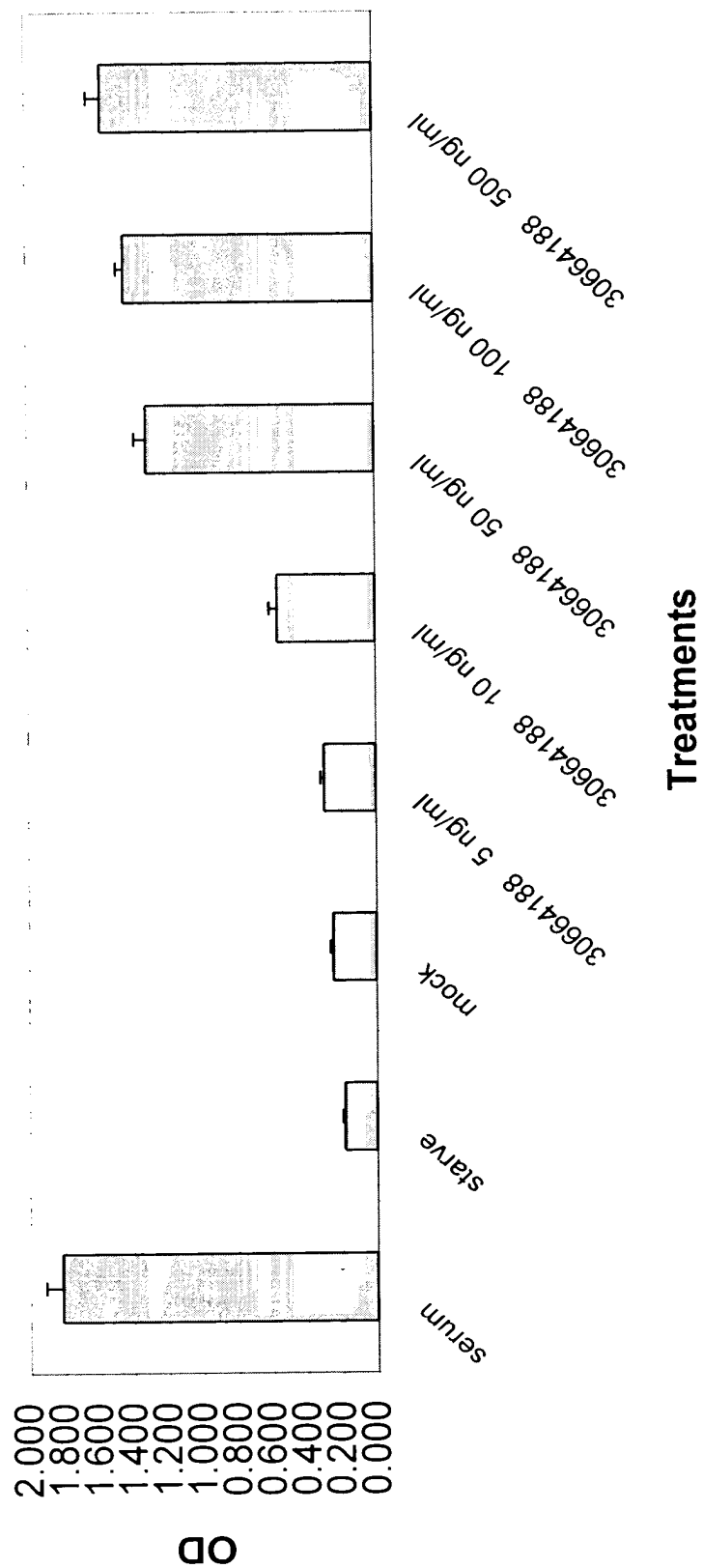


FIG. 7.

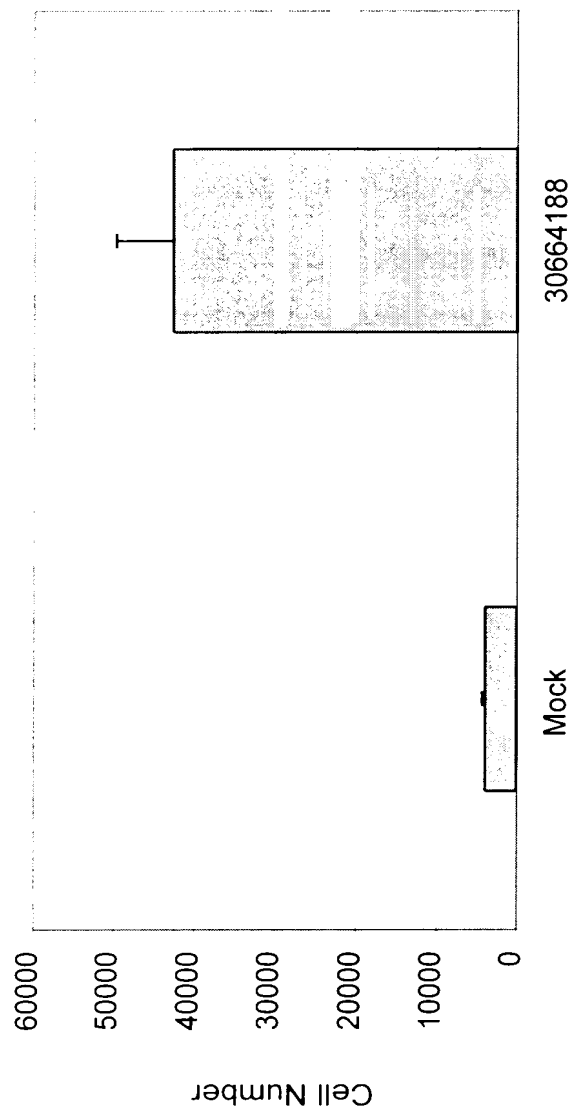




FIG. 9.

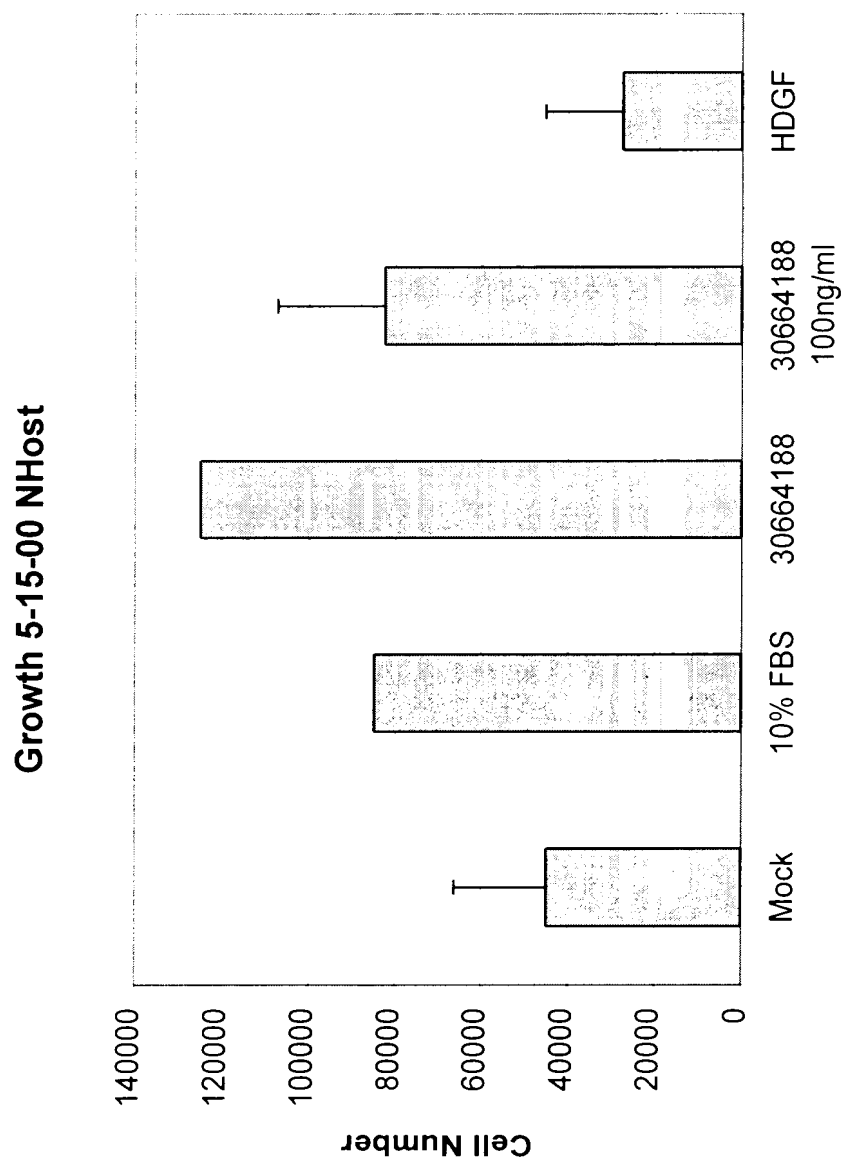




FIG. 10.

FIG. 10A (without serum)

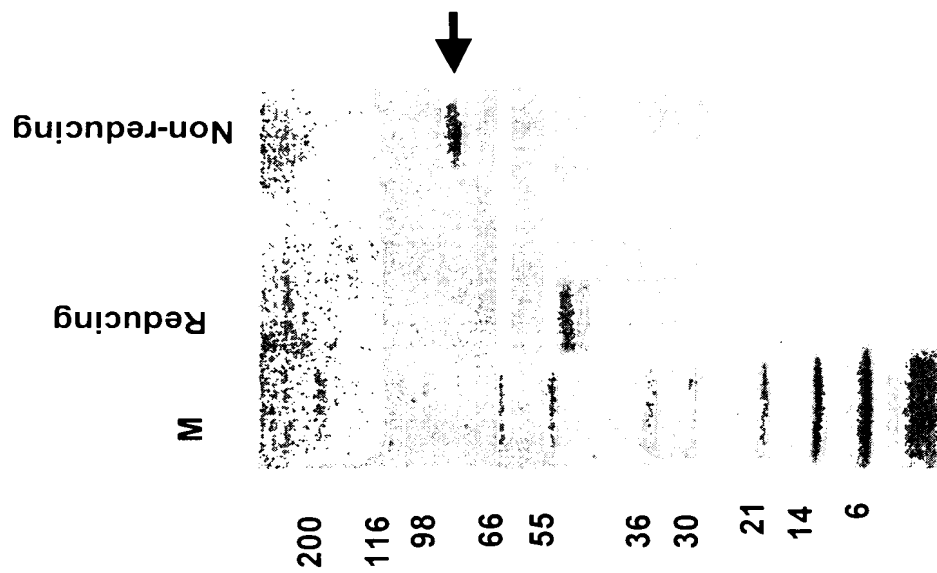


FIG. 10B (with serum)

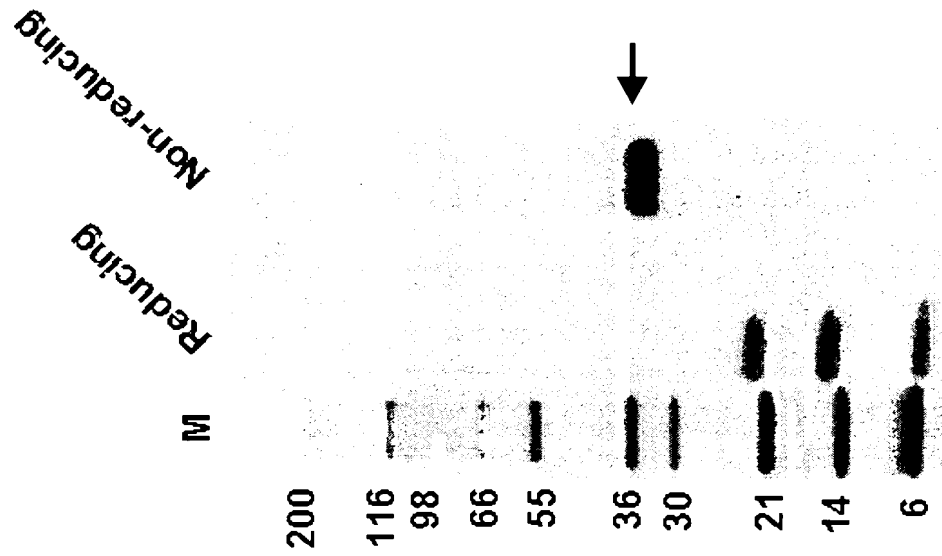


FIG. 11.

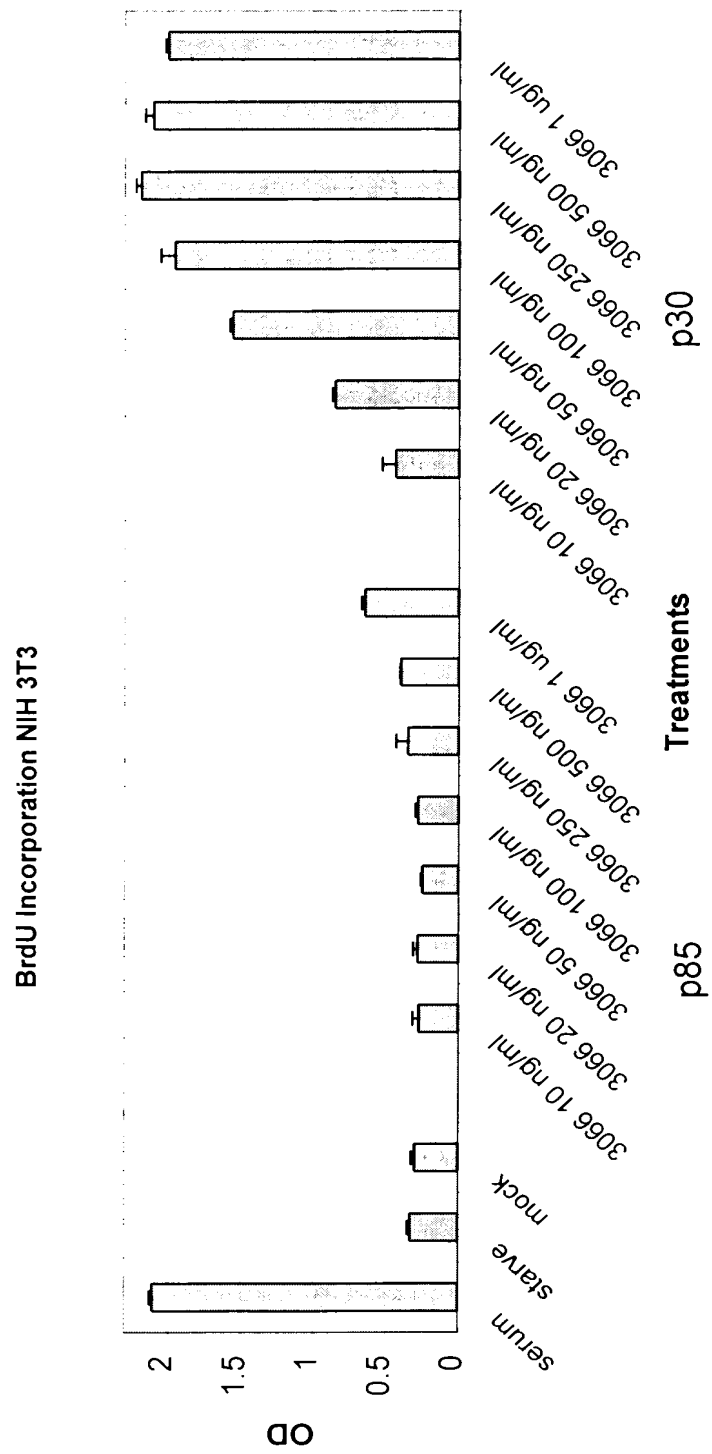



FIG. 12

			*
hPDGF D	CTPRNYSVNI-REELKLANVVF--FPRCLLVQRCGGNCGCGTVNWR	SCTC	
mPDGF D	CTPRNHSVNL-REELKLTNAVF--FPRCLLVQRCGGNCGCGTVNWK	SCTC	
PDGF C	CTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACCLHNC	NECQC	
PDGF B	CKTRTEVFESISRLIDRTNANFLVWPPC	VEVQRCSG--CCNNRNVQCRP	
PDGF A	CKTRTVIYEIPRSQVDPTSANFLIWPPC	VEVKRCTG--CCNTSSVKCQP	
hPDGF D	NS---GKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHER	CDC	(SEQ ID NO:15)
mPDGF D	SS---GKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHER	CDC	(SEQ ID NO:16)
PDGF C	VP---SKVTKKYHEVLQLRPKTGVRGLH-KSLTDVA--LEHHEE	CDC	(SEQ ID NO:17)
PDGF B	TQVQLRPVQVRKIEIVRKKPIF-----KKAT-VT----LEDH	LACKC	(SEQ ID NO:18)
PDGF A	SRVHHRSVKVAKVEYVRKKPKL-----KEVQ-VR----LEE	HLECAC	(SEQ ID NO:19)

FIG. 13

1  Exon 1  
 81 AATGACCGGGTTCATCTTTGTCTACACTCTAATCTGGGCAAACTTTTGCAGCTGTGGGGACACTTCTGCAACCGGGCAGA  
 M H R L I F V Y T L I C A N F C S C R D T S A T P Q S  
 161 GGGCATCCATCAAAGCTTTGGGCAACGGCAACCTCAGGGGAGATGAGAGCAATCACTCAGAGACTTGTACCGAAGAGAT  
 A S I K A L R N A N L R R D E S N H L T D L Y R R D  
 241 GAGACCATCCAGGTGAAAGGAAACGGCTACGTGCAGAGTCTTAGATTCCCGAACAGCTACCGCCAGGAACCTGCTCCTGAC  
 E T I Q V K G N G Y V Q S P R F P N S Y P R N L L L T  
 321 ATGGGGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTTGACAATCAGTTTGGATTAGAGGAAGCAGAAAATG  
 W R L H S Q E N T P I Q L V F D N Q F G L E E A E N D  
 401 ATATCTGTATGATGATTTTGTGGAAAGTTGAAGATATATCCGAAACAGTACCATATTAGAGGAGGATGGTGTGGACAC  
 I C R Y D F V E V E D I S E T S T I I R G R W C G H  
 481 AAGGAAGTTTCTCCAAAGGATAAAATCAAGAAACGAACCAAAATTAATCAACATTCAAGTCCGATGACTACTTTTGTGGCTAA  
 K E V P P R I K S R T N Q I K I T F K S D D Y F V A K  
 561 ACGTGGATTCAAGATTTATTATCTTTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGAACCACTGGGAATCTGTCA  
 P G F K I Y Y S L L E D F Q P A A A S E T N W E S T  
 641 CAAGCTCTATTTCAGGGGTATCTTATAAATCTCTCCATCAGTAACGGATCCCACTCTGATTGGGGATGCTCTGGACAAAAA  
 S S I S G V S Y N S P S V T D P T L I A D A L D K K  
 721 ATTGCAGAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCAATGGCAAGAAGATCTTGAGAATATGTA  
 I A E F D T V E D L L K Y F N P E S W Q E D L E N M Y  
 801 TCTGGACACCCCTCGGTATCGAGGCAGGTCAATCCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATG  
 L D T P R Y R G R S Y H D R K S K V D L D R L N D D A  
 881 CCAAGCGTTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAAATGTGGTCTTTCTTT  
 K R Y S C T P R N Y S V N I R E E L K L A N V V F F  
 961 CCAAGTTGGCTCCTCTGTCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACTGTCAACTGGAGGTCTGTCACATGCAATTC  
 P R C L L V Q R C G G N C G C G T V N W R S C T C N S  
 1041 AGGGAAAAACCGTGAAGAAAGTATCATGAGTATTACAGTTTGGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCA  
 G K T V K K Y H E V L Q F E P G H I K R R G R A K T M  
 1121 TGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATGTGATTGTATCTGCAGCTCAAGACCACTCGATAAGAGAAT  
 A L V D I Q L D H H E R C D C I C S S R P P R (SEQ ID NO:20)  
 1201 GTGCACATCCTTACATTAAGCGTGAAGAAACCTTTAGTTTAAAGGAGGGTGAGATAAGAGACCCCTTTTCTACCCAGCAACC  
 1281 AAACCTTACTACTAGCCTGCAATGCAATGAACACAAGTGGTGTGCTGAGTCTCAGCCTTGTCTTTGTTAATGCCATGGCAAGT  
 1361 AGAAAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAATAGTGTGAGGTTATATATGCACAA  
 1441 ACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAATGTTTTTTTTTGGTATATATAACCGAGGTACACAGAG  
 1521 CTTACATATGTTTGAAGTAGACTCTTAAATCTTTGGCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAA  
 1601 AATTTAGGAGATAAATTTATTTTTAAATTTTGAACACAAAACAATTTGAATCTTGTCTCTTAAAGAAAGCATCTTGT  
 1681 ATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:21)








Exon 1  Exon 2  
 Exon 2  Exon 3  
 Exon 3  Exon 4  
 Exon 4  Exon 5  
 Exon 5  Exon 6  
 Exon 6  Exon 7  
 Exon 7 

FIG. 14

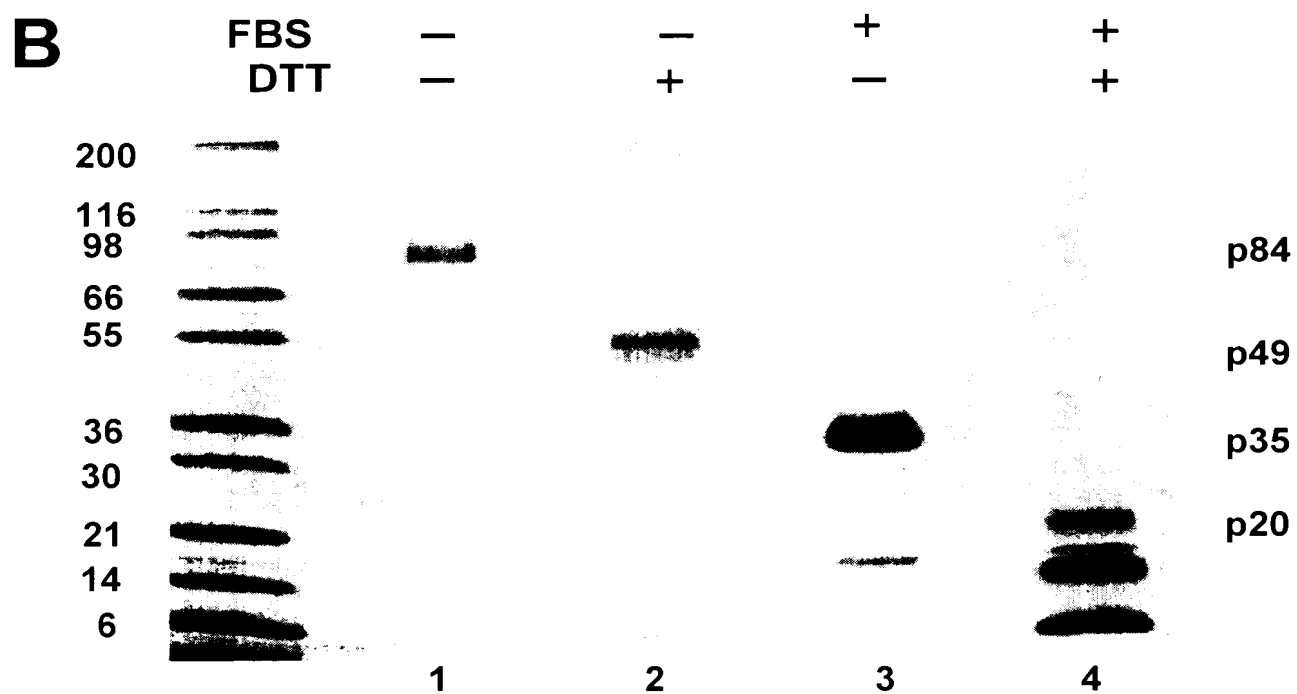
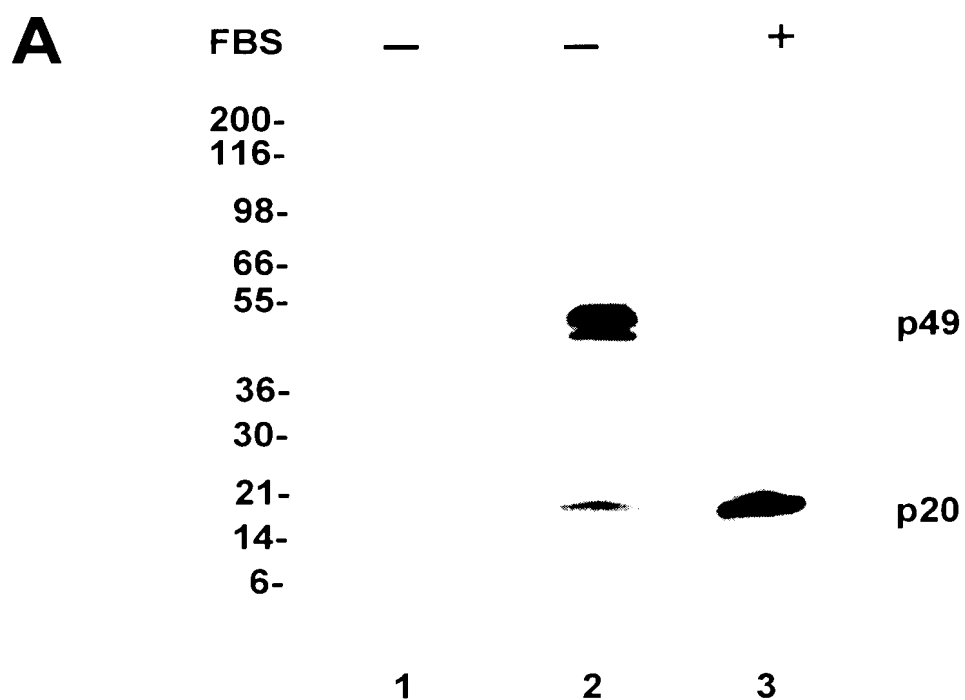


FIG. 15

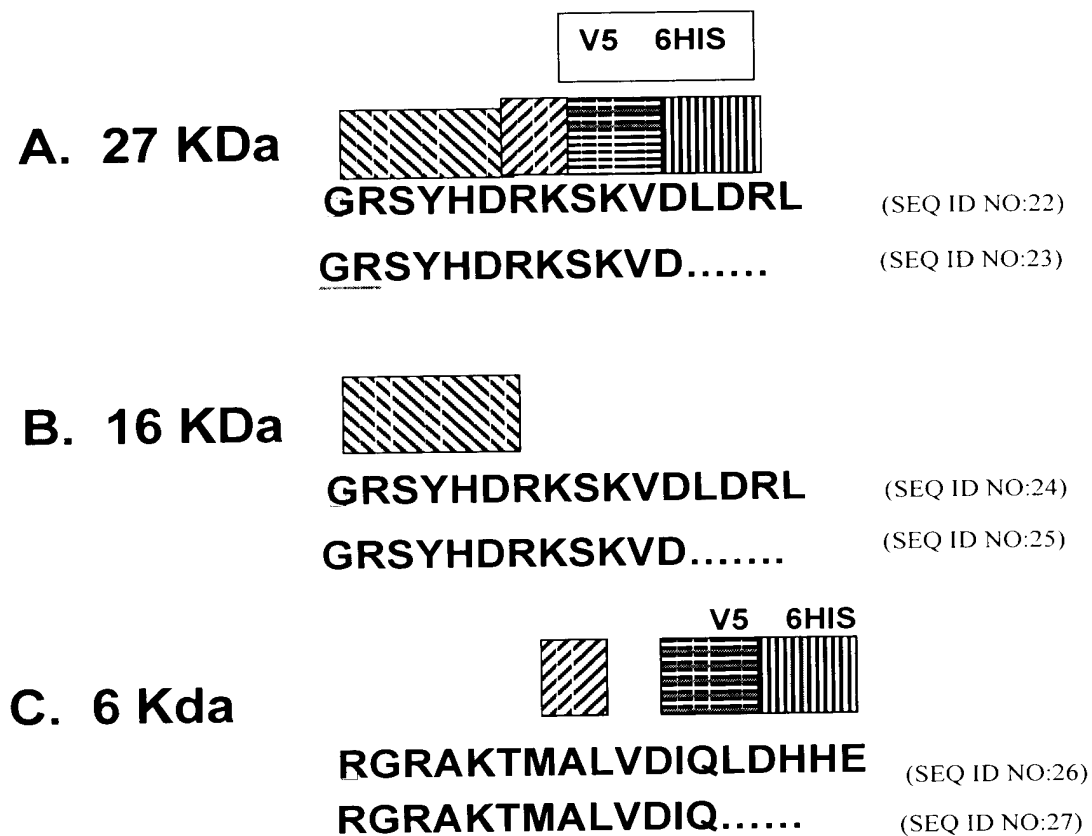


FIG. 16

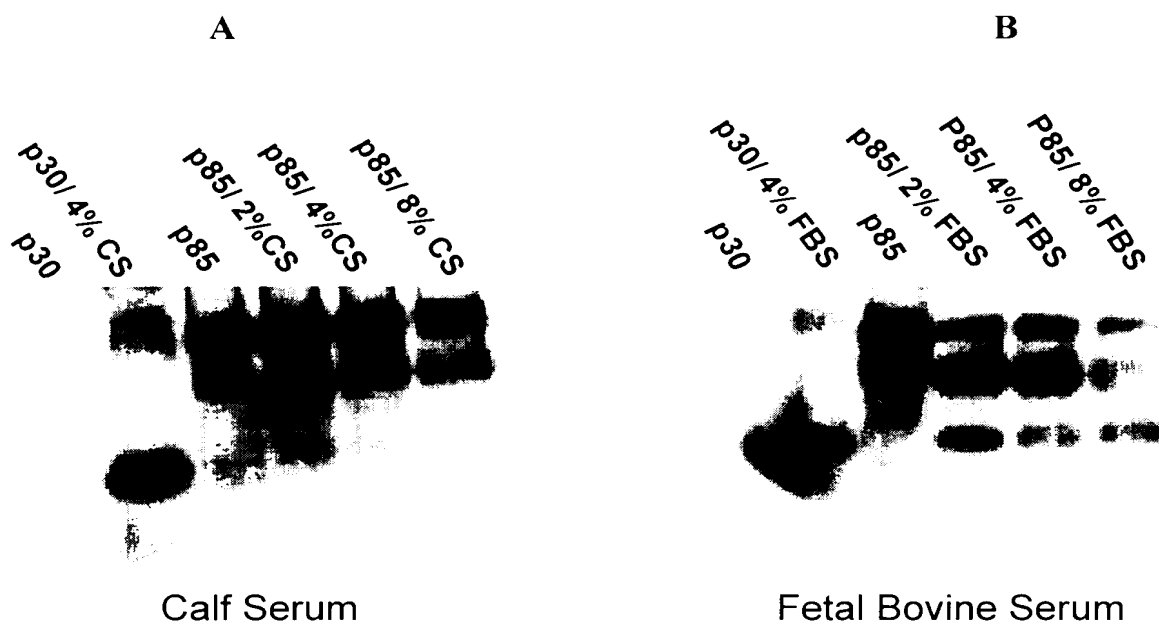


FIG. 17

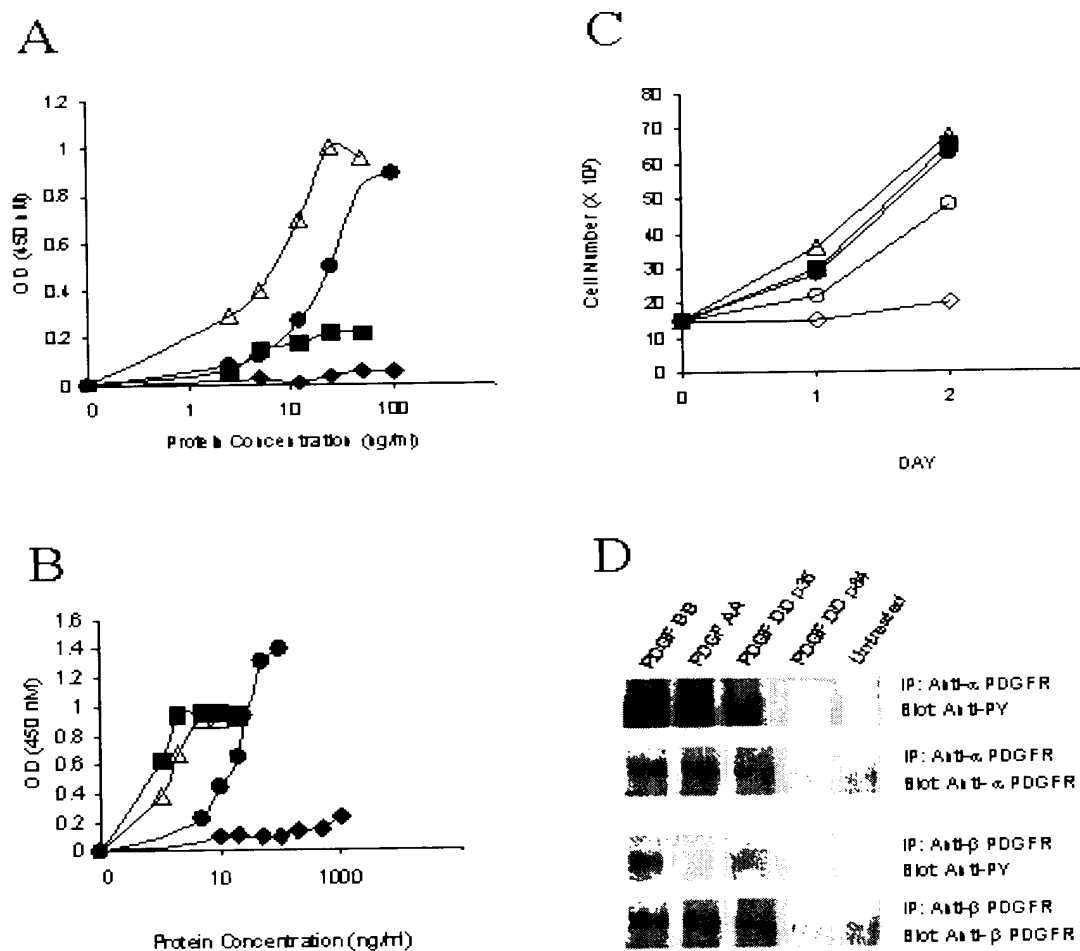
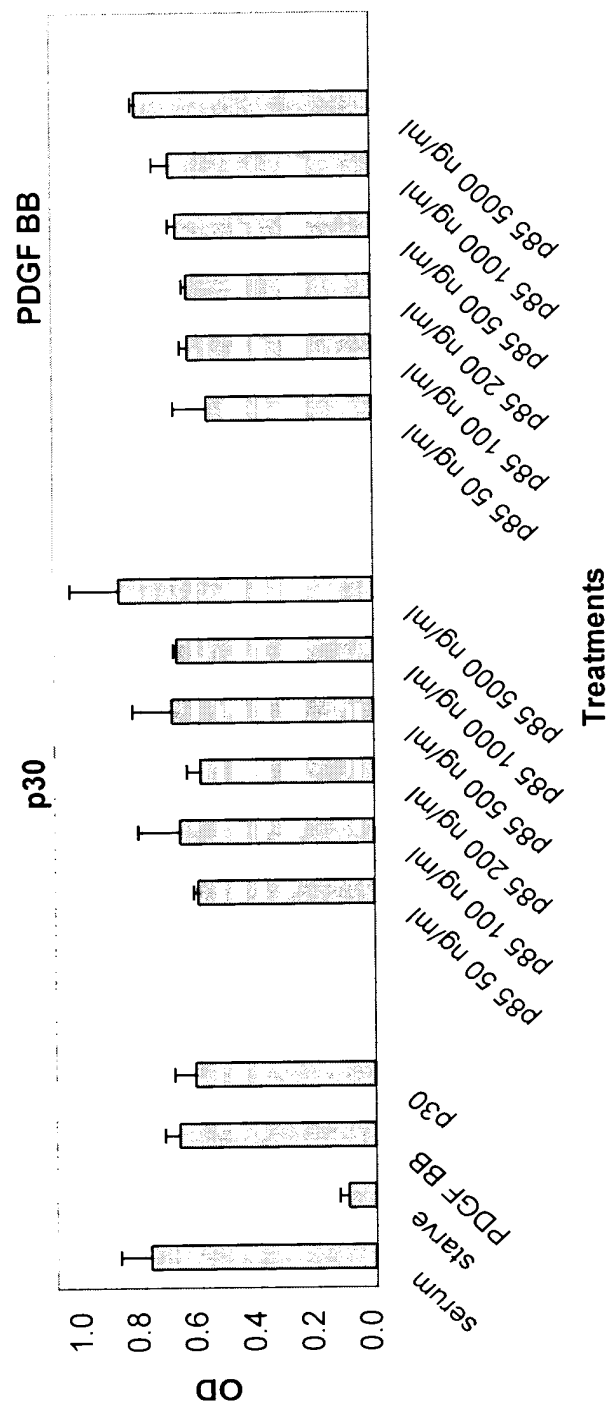




FIG. 18

Competition of 30664188 p30 or PDGF BB by 30664188 p85



A

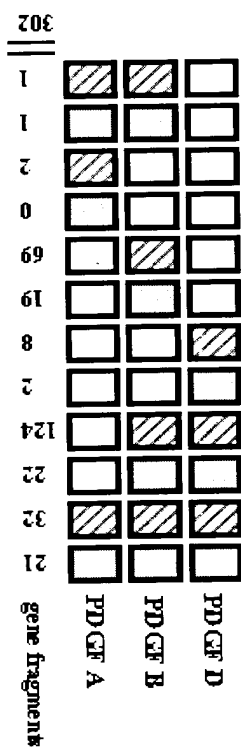


FIG. 19

FIG. 20

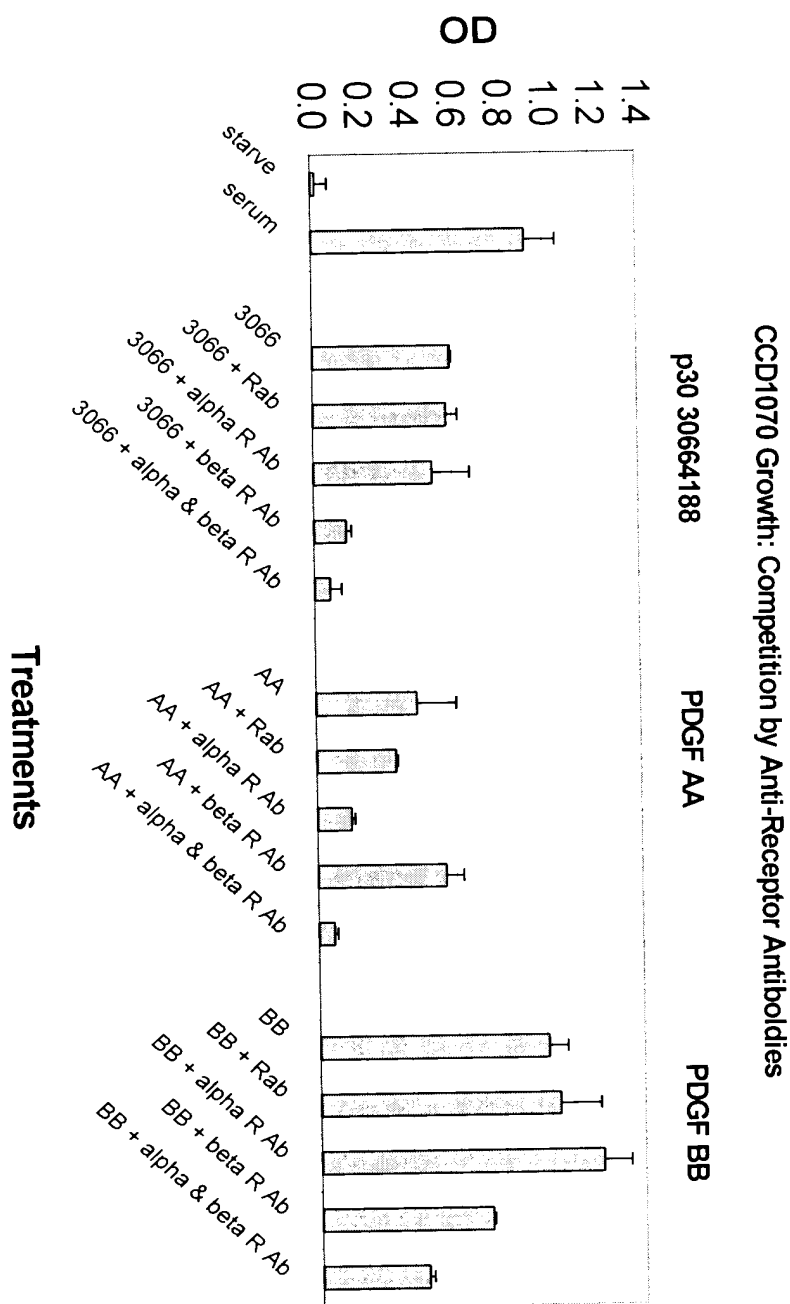


FIG. 21

Smooth Muscle Treated with p30 30664188, PDGF AA, PDGF BB

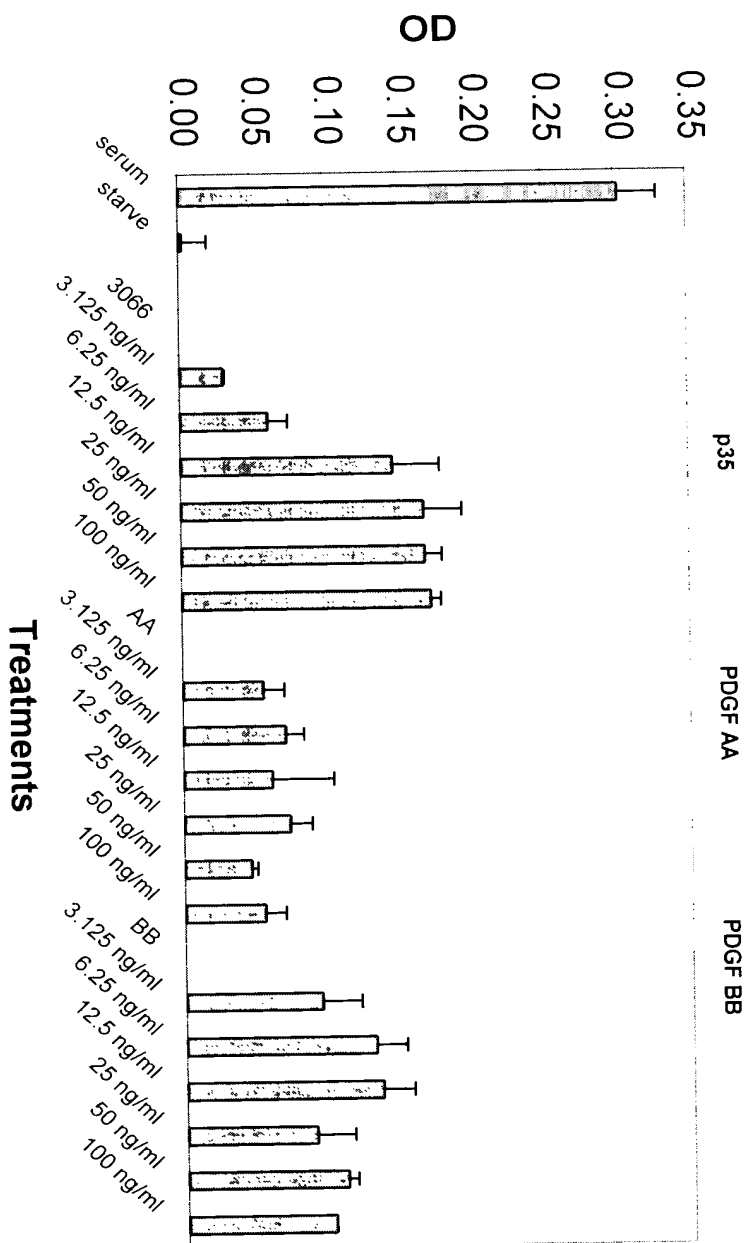


FIG. 22

### Smooth Muscle Cell Proliferation

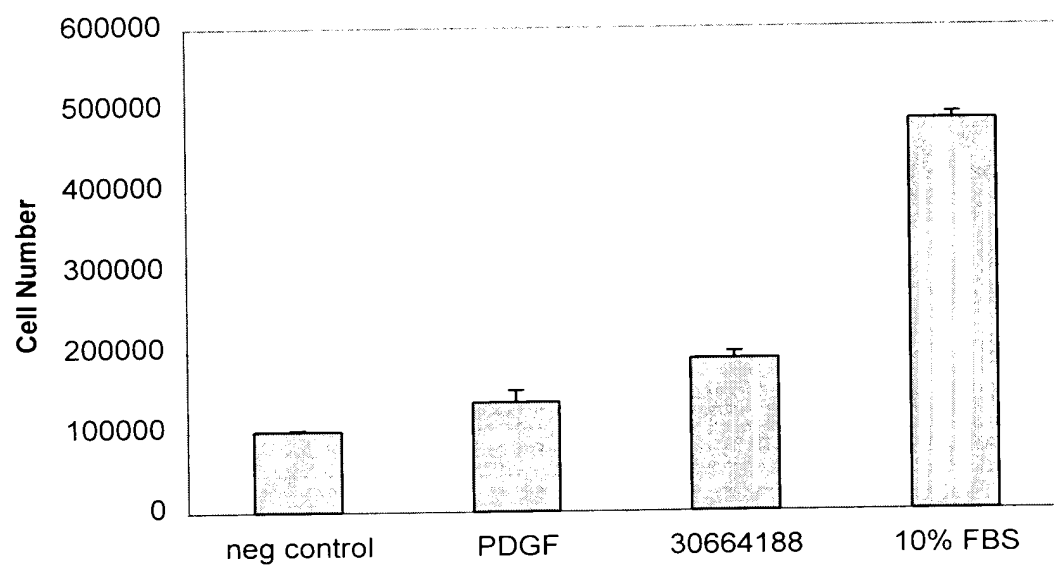


FIG. 23

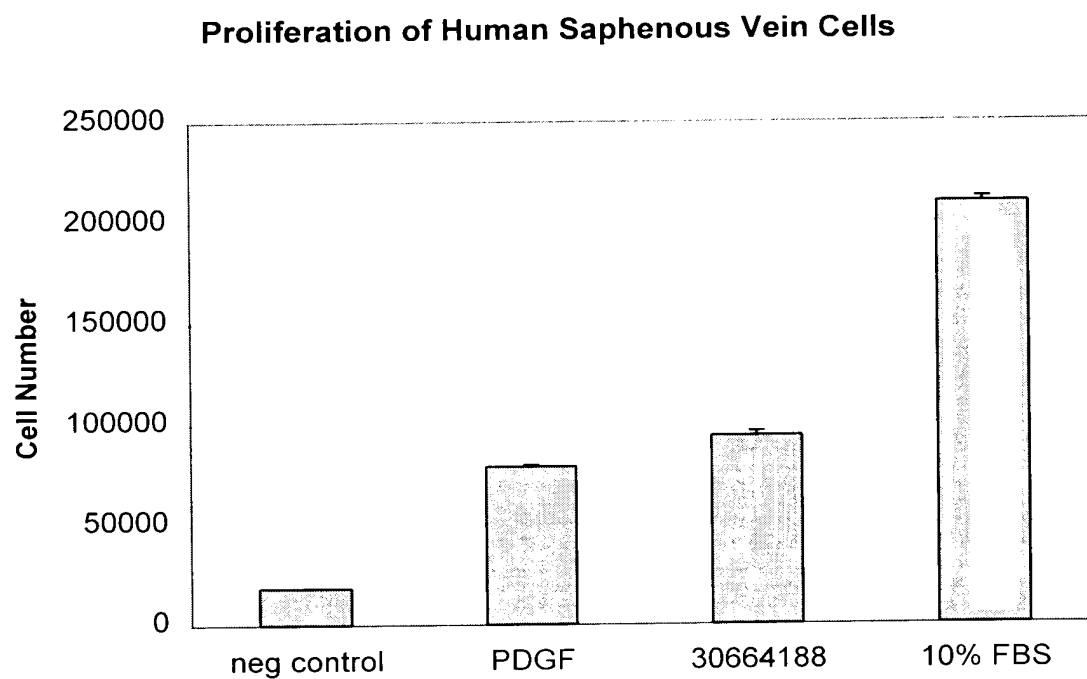


FIG. 24

# Neutralization of 30664188 by Fully Human Polyclonal Ab

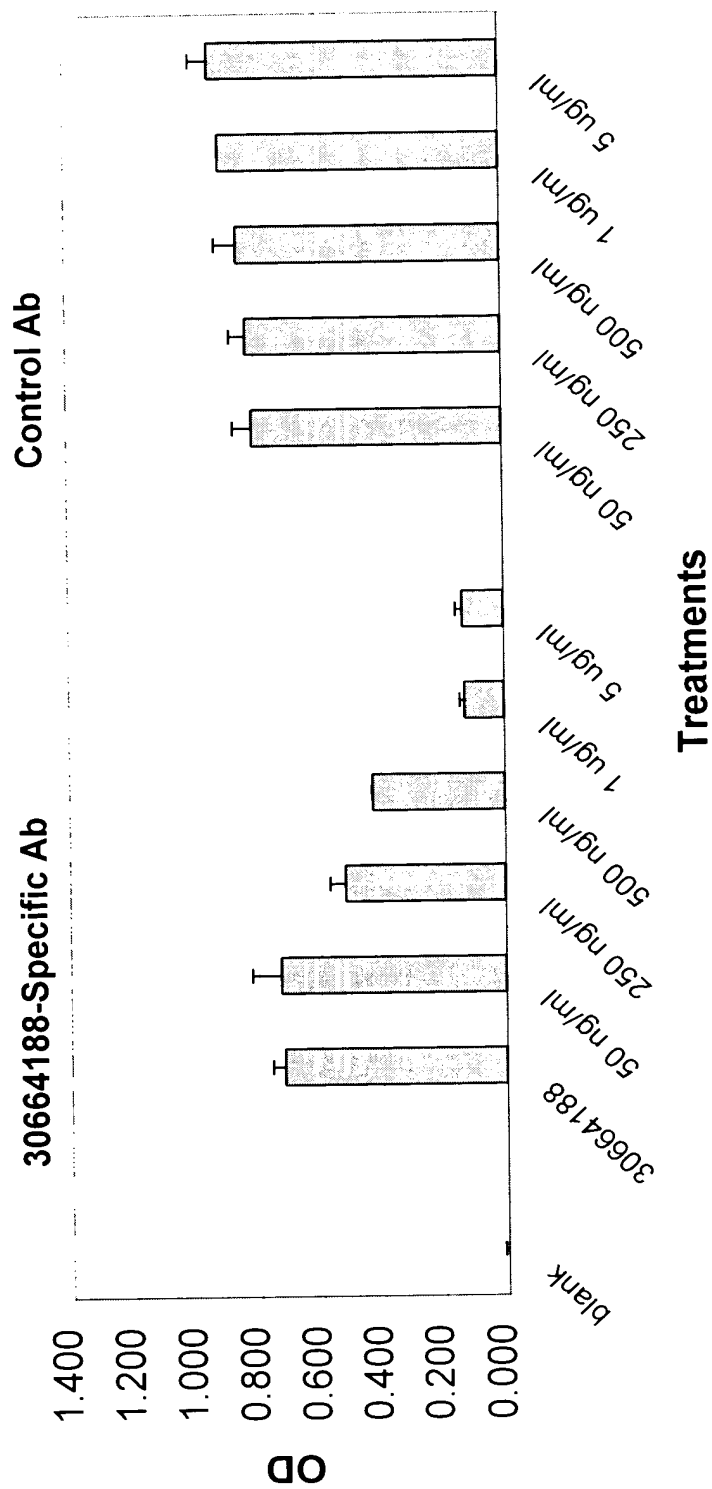


Fig. 25.

Panel A

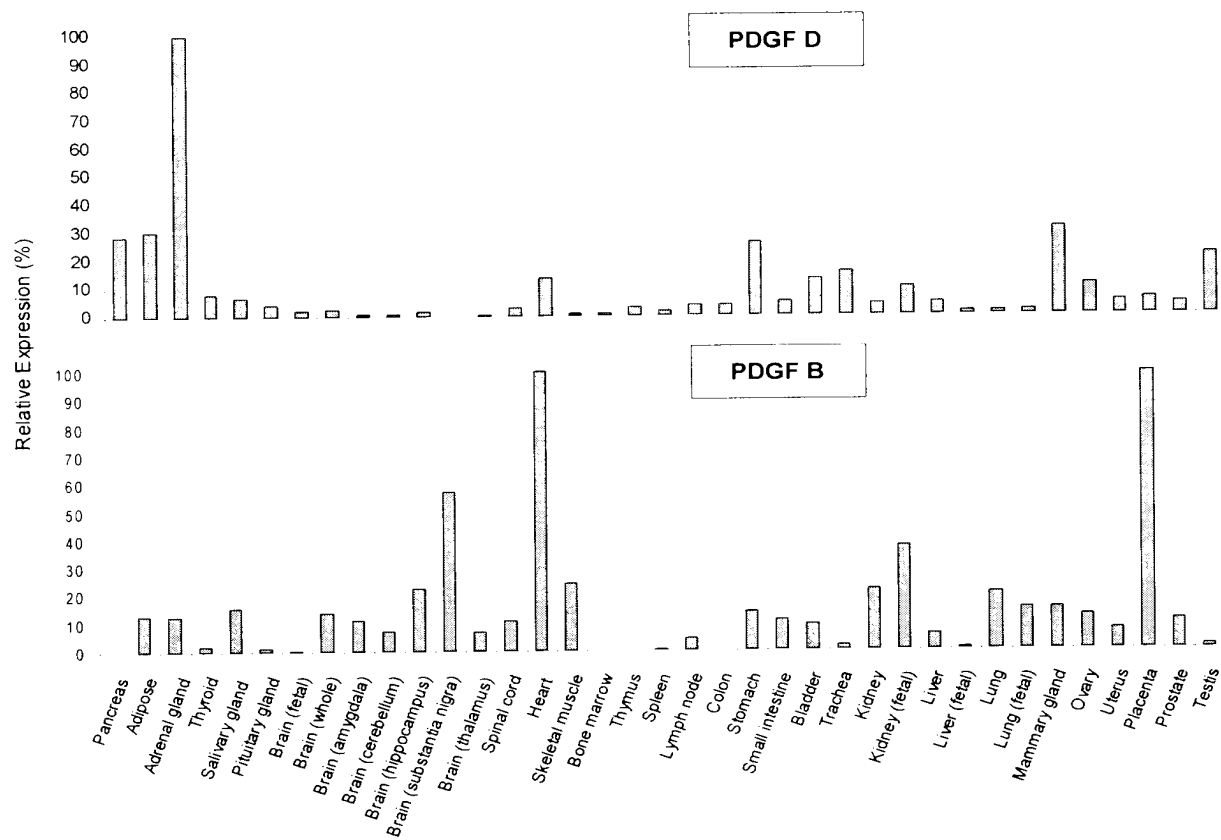




Fig. 25 (cont.)

Panel B

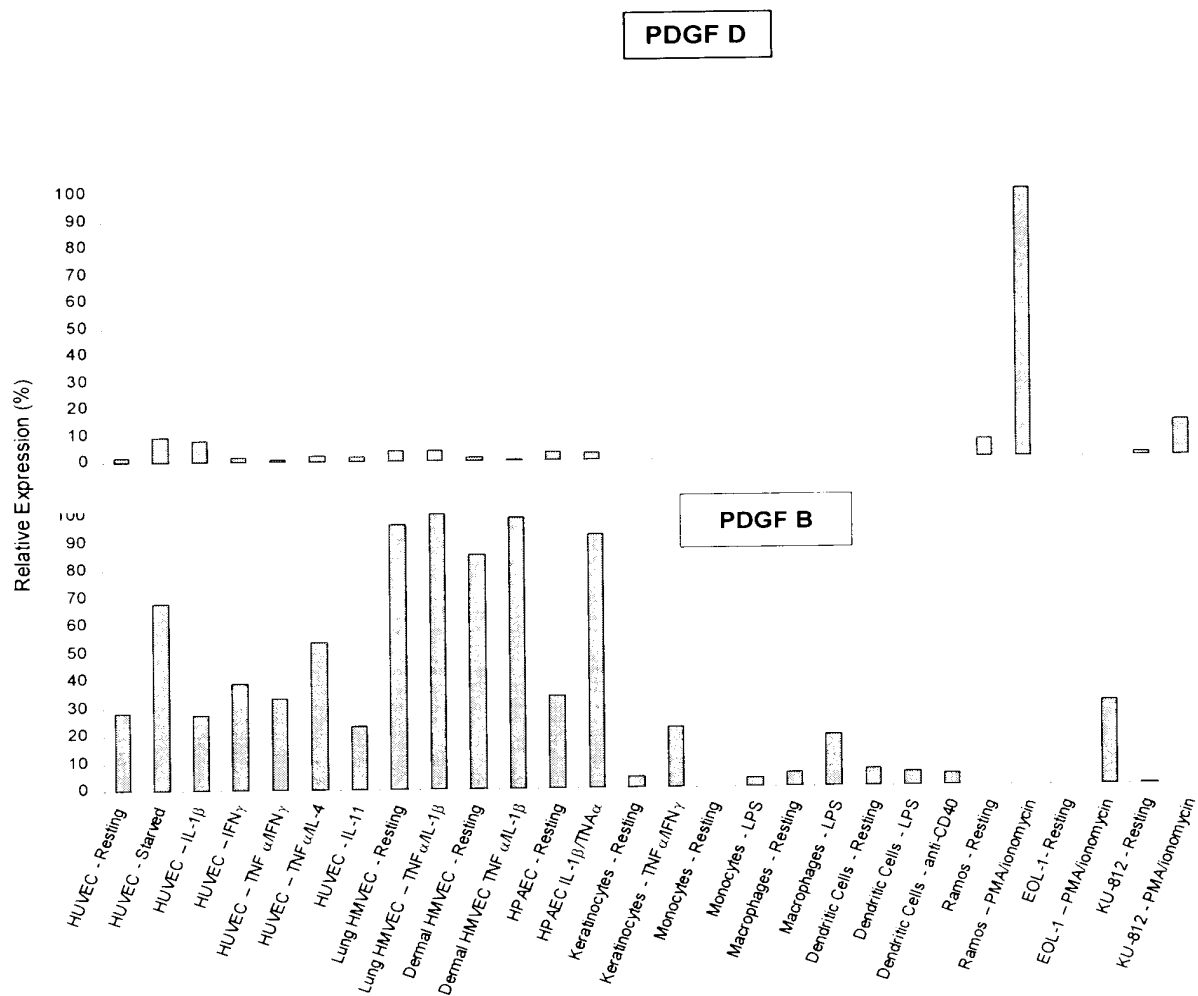


FIG. 26.

# BrdU CCD1070 Soluble Alpha PDGFR Competition

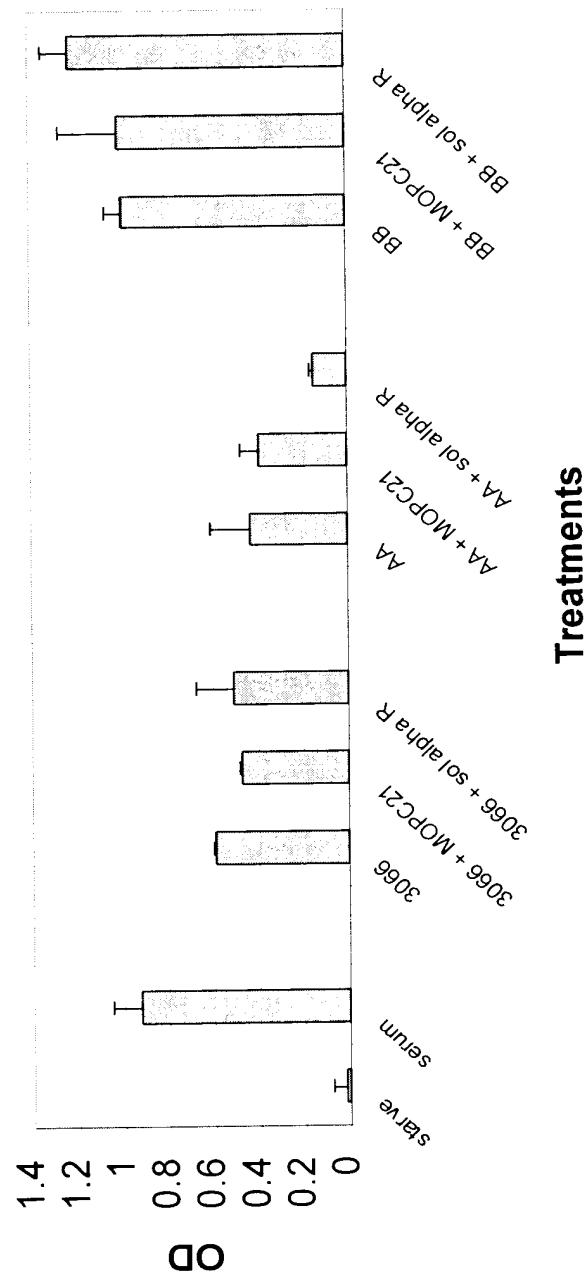


FIG. 27A

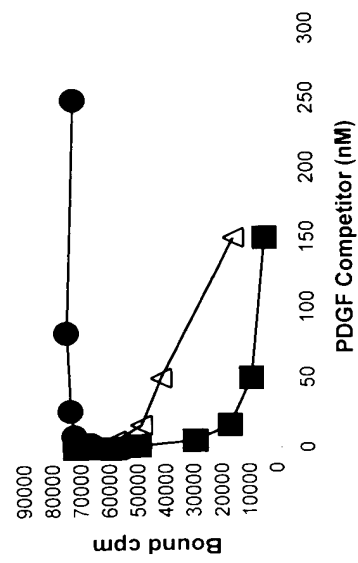


FIG. 27B

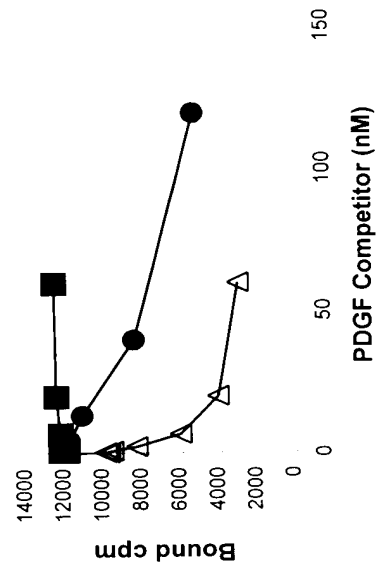


FIG. 28

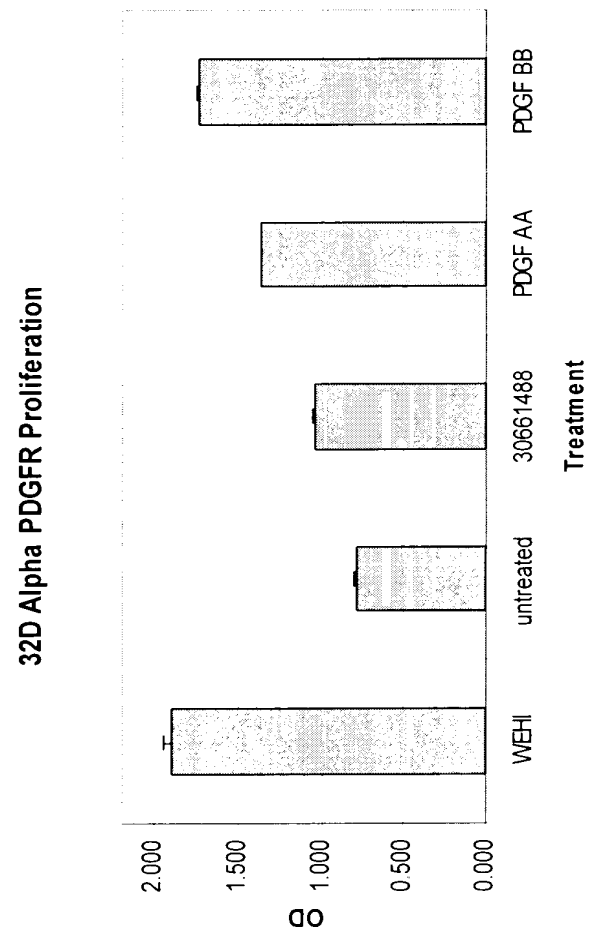


FIG. 29A

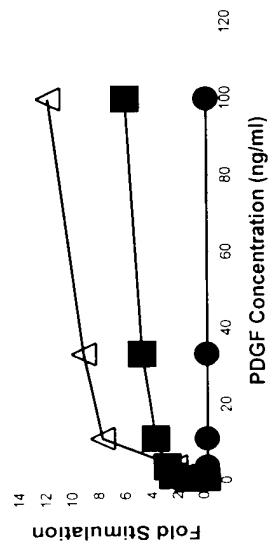


FIG. 29B

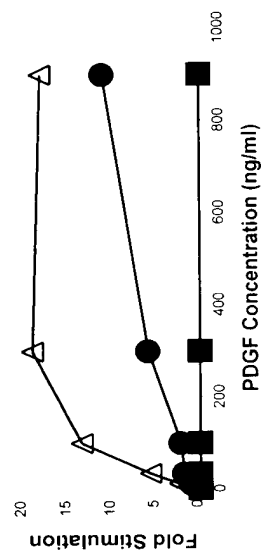


FIG. 29C

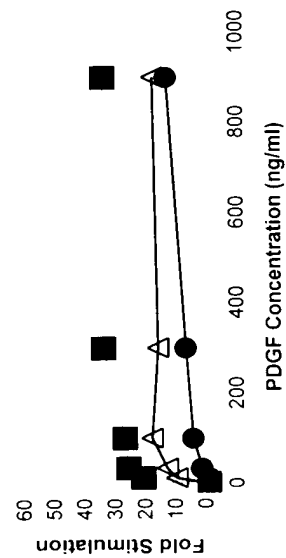


FIG. 29D

